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Application of Subspace Method and Sparse Coding to Tissue Characterization of Coronary Plaque for High-Speed Classification

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Abstract

The major cause of Acute Coronary Syndrome (ACS) is a rupture of coronary plaque. Therefore, the tissue characterization of coronary plaque is important for a diagnosis of ACS. In this study, we propose a method to use sparse features and its neighboring information obtained by a sparse coding. In the proposed method, the Radio Frequency (RF) signal obtained by the IntraVascular UltraSound (IVUS) method is expressed by a linear combination of the basis functions extracted from the learning signals by the sparse coding, and the code patterns of the expansion coefficients of the basis functions are used for the tissue characterization. In addition, in order to perform a high-speed tissue characterization, the subspace method is employed as the classifier. The effectiveness of the proposed method has been verified by comparing the classification results of the proposed method with those of the frequency analysis-based conventional method applying to the data obtained from the human coronary arteries.

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Keywords: sparse coding; tissue characterization; coronary plaque; subspace method.

1. Introduction

Acute Coronary Syndrome (ACS) is caused by the rupture of plaque formed in coronary artery. To diagnose the plaque, the property of the plaque and its structure need to be identified. The major method, for the present, to get the information about the condition of the coronary artery is the IntraVascular UltraSound (IVUS) method. The ultrasound signal is emitted from the probe attached to the end of a catheter, and its reflected signal from the tissue of the plaque is again received by the probe. This ultrasound signal is called a Radio Frequency (RF) signal, which is analyzed by the computer to diagnose the plaque.

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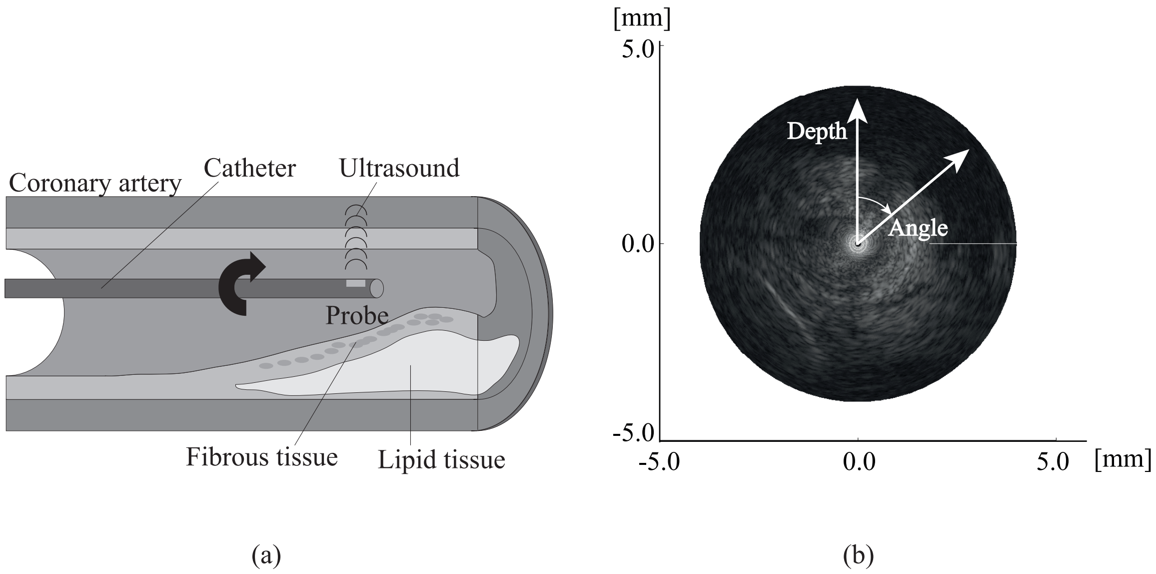


Fig. 1. (a) An ultrasound probe attached to the distal end of a catheter. The ultrasound signal is emitted from the probe and the reflected signal from the tissue is received again by the probe. (b)An example of the B-mode image constituted by the RF signal (reflected ultrasoud signal). This is a real time cross-sectional image of a blood vessel where a catheter probe is currently rotating.

The cross-sectional image of the blood vessel is constituted by the reflected RF signal. This image is called a B-mode image[1]. In general, a medical doctor diagnoses the plaque using this B-mode image. It is difficult however to diagnose the property of the plaque just by observing this B-mode image.

There are two major methods to identify (classify) the tissue of plaque. One method is Integrated Backscatter (IB) method[2,3]. Another method is based on the frequency analysis of RF signal[4]. In the IB method, it is however difficult to classify the tissue of plaque, because the IB value changes according to the distance between the probe and the plaque. On the other hand, as for the method based on the frequency analysis, the classification accuracy is not enough, because the frequency characteristics of tissue are not so clearly splitted.

In this paper, we propose a novel method to classify the tissue of coronary plaque using the coefficients pattern obtained by sparse coding[5,6]. The originality of the proposed method is an introduction of the sparse coding to a subspace-based classifier. In the proposed method, in order to perform a high-speed tissue characterization, the subspace method is employed as a classifier. The effectiveness of the proposed method is verified by some experiments.

2. Conventional Tissue Characterization Method

2.1. IVUS Method

The IVUS method is one of the medical imaging techniques. In the IVUS method, the catheter with the ultrasound probe attached to its distal end is inserted and then rotated in the coronary artery (Fig. 1 (a)). The ultrasound signal is emitted from the probe, and the RF signal reflected from the tissue is received also by the probe. The emitting frequency of the ultrasound is 40 MHz, and the RF signal is sampled at 400 MHz.

An IVUS B-mode image[7] is constituted by analyzing by the received RF signal (Fig. 1 (b)). This IVUS B-mode image expresses a tomographic image of the cross-section of the coronary artery. This image is constructed with 2,048 points in depth, and 256 lines in radial direction.

2.2. IB Analysis

In the IVUS-based conventional tissue characterization methods, the IB analysis is a typical method. In this analysis, the tissue is classified only by the IB value (IBS) calculated by[2]:

$$\mathrm{IBS} = 20\log\left(\frac{\frac{1}{T}\int_0^T V^2 dt}{\frac{1}{T}\int_0^T V_0^2 dt}\right), \tag{1}$$

where V is a signal from a region of interest, V_0 is the smallest signal that the system can detect, and T is an integration interval. In the IB analysis, the threshold of the IB value is set for the classification of the fibrous and lipid tissues so that the learning signals are most precisely classified.

The IB analysis is simple, and is effective in a restricted case. However, it is not always accurate to classify the tissues of plaque, because some types of tissue have similar IB values with each other. Moreover, the strength of the IB value changes according to the distance between the probe and the tissue. This is a fatal defect of the IB analysis.

2.3. Frequency Analysis

The frequency analysis of RF signal is another approach for the tissue characterization. In this method, the normalized power spectrum of the local RF signal is used as the feature vector. However, since the frequency characteristics of some tissues are similar to others, a precise tissue classification is not yet achieved.

3. Tissue Characterization Method by Sparse Coding

3.1. Sparse Coding

The sparse coding is a method to represent a signal by a few basis functions imitating the perceptual system of the mammalian visual cortex. The sparse coding was first proposed by B. A. Olshausen and D. J. Field[5]. The algorithm for learning overcomplete sparse codes is described in the reference[6]. It is closely related to the Independent Component Analysis (ICA)[8,9], which is well known as a statistical method to estimate the underlying features of the observed signal. We try to apply the high feature extraction ability of the sparse coding to the tissue characterization. Here, the RF signal is treated as a two dimensional signal by considering the depth and radial directions. In the proposed method, the sparse code patterns obtained are used as the feature vectors.

3.1.1. Representation of RF signal

A local RF signal $\boldsymbol{x}$ in a short time interval is represented by a linear combination of the basis functions $\boldsymbol{\phi}_i$ as follows:

$$\boldsymbol{x} = \sum_{i=1}^{M} a_i \boldsymbol{\phi}_i, \tag{2}$$

where a_i is the expansion coefficient for each basis function $\boldsymbol{\phi}_i$, and M is the number of the basis functions. $\boldsymbol{x}$ and $\boldsymbol{\phi}_i$ are the following vectors:

$$\boldsymbol{x} = (x_1, \ldots, x_L)^t, \tag{3}$$

$$\boldsymbol{\phi}_i = (\phi_{i1}, \ldots, \phi_{iL})^t, \tag{4}$$

where L is the dimension of $\boldsymbol{x}$ sampled in the short time interval, and t is a transpose operation.

3.1.2. Cost function of sparse coding

The basis functions $\boldsymbol{\phi}_i$ and the coefficients a_i are statistically determined by a set of the local RF signals $\boldsymbol{x}$, which are cut out randomly from the learning signals. $\boldsymbol{\phi}_i$ and a_i are estimated by using the local RF signals $\boldsymbol{x}$.

In the sparse coding, the following cost function is employed to determine the basis functions $\boldsymbol{\phi}_i$ and the coefficients a_i[5,6]:

$$E = \left\langle \sum_{j=1}^{L} \left(x_j - \sum_{i=1}^{M} a_i \phi_{ij} \right)^2 + \beta \sum_{i=1}^{M} S\left(\frac{a_i}{\sigma}\right) \right\rangle, \tag{5}$$

where $< \cdot >$ is an averaging operator, and β is a positive constant. σ is a scaling constant. The standard deviation of the learning signals is used as σ. $S(y)$ is an arbitrary nonlinear function.

The first term of Eq. (5) indicates the signal reconstruction performance by evaluating the sum of the square error between the input signal x_j and the reconstructed signal represented by a linear combination of $\boldsymbol{\phi}_i$. The second term determines the sparseness of the expansion coefficients a_i. In this paper, $\log(1 + y^2)$ is used as the nonlinear function $S(y)$.

3.1.3. Learning algorithm of sparse coding

The learning algorithm of the sparse coding results in minimizing Eq. (5) with respect to a_i and $\boldsymbol{\phi}_i$. That is, the updating rule of a_i is given by:

$$\Delta a_i = b_i - \sum_{k=1}^{M} R_{ik} a_k - \frac{\beta}{\sigma} S'\left(\frac{a_i}{\sigma}\right) \tag{6}$$

with

$$b_i = \sum_{j=1}^{L} \phi_{ij} x_j, R_{ik} = \sum_{j=1}^{L} \phi_{ij} \phi_{kj}, \tag{7}$$

where Δa_i is an updated value of a_i and $S'(y)$ is a differential of $S(y)$.

The updating rule of $\boldsymbol{\phi}_i$ is given by:

$$\Delta \phi_{ij} = \eta \left\langle a_i \left(x_j - \sum_{i=1}^{M} a_i \phi_{ij} \right) \right\rangle, \tag{8}$$

where η is a learning rate.

a_i are updated according to Eq. (6) every time when each input signal is applied, and ϕ_{ij} are updated when after 100 input signals are applied.

3.1.4. Feature extraction

The followings are the characteristics of the basis functions $\boldsymbol{\phi}_i$ and the coefficients a_i obtained from the learning signals by sparse coding.

(i) The frequency characteristics of the signals reconstructed by the basis functions $\boldsymbol{\phi}_i$ and those of the learning signals are similar to each other.
(ii) The code pattern (pattern of a_i) is sparse.

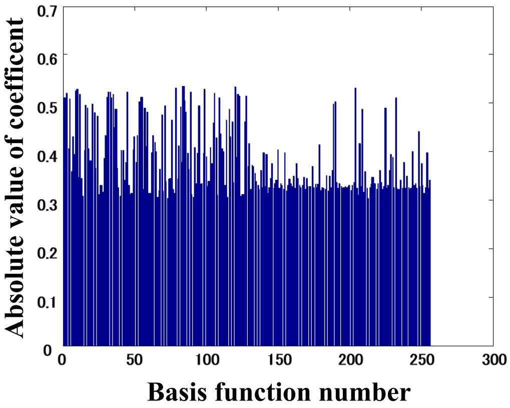
In this paper, we use a code pattern as a feature vector of the RF signal for the tissue characterization.

3.2. Classification

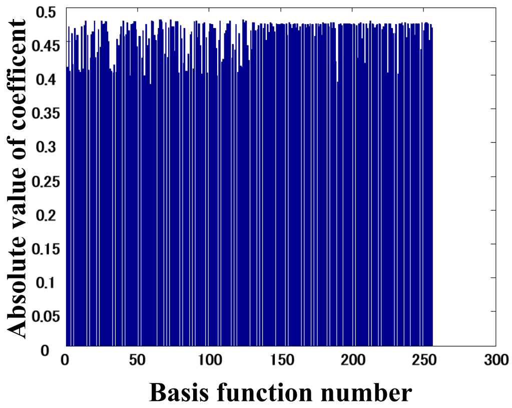
The proposed method classifies the tissues of plaque by using the sparse code patterns of a_i. The basis functions for the sparse coding are first extracted from the learning signals reflected from the fibrous and lipid tissues. Next the local RF learning signals of the fibrous tissue are represented by the basis functions. The code patterns obtained are used as the training vectors with the class label of the fibrous tissue. In the same way, the training vectors with the class label of the lipid tissue are obtained from the learning signals of the lipid tissue. The set $\boldsymbol{A}$ of the training vectors is given as follows:

$$\boldsymbol{A} = (\boldsymbol{a}_1, \ldots, \boldsymbol{a}_N), \tag{9}$$

where N is the number of the training vectors with the class label of fibrous or lipid tissue.



(a)



(b)

Fig. 2. Average of absolute value of the sparse code patterns. (a)Fibrous tissue. (b)Lipid tissue.

The target local RF signal, where its tissue is unknown, is represented by the basis functions, and then the tissue characterization is performed by applying a classifier with training vectors $\boldsymbol{A}$. We realized, in the previous works [10], the accurate tissue characterization by using those feature vectors with K-Nearest Neighbor (KNN) [11,12]. KNN however takes much time to calculate the distance between an unknown vector and the training vectors.

Figure 2 shows each average of the absolute value of the sparse code patterns for each tissue. It is observed that the ignited bases for each tissue are different. From these results, the feature vectors obtained by sparse coding are considered to be independent between each class. It is thus highly possible to perform accurate tissue characterization in a high-speed by using the subspace method [13] with those feature vectors.

3.3. Subspace Method

In the subspace method in general, the subspaces are constructed for each class to be classified. This subspace is used to calculate the similarities between an unknown vector and the vectors of each class. The unknown vector is classified into the corresponding class based on this similarity.

Now consider c subspaces $\boldsymbol{Q}_1, \boldsymbol{Q}_2, \cdots, \boldsymbol{Q}_c$ for class $\omega_1, \omega_2, \cdots, \omega_c$. The subspace $\boldsymbol{Q}_i$ of class ω_i is constructed by the basis vectors obtained by the training vectors of class ω_i. The basis vectors are calculated by the Principal Component Analysis (PCA). In PCA, the eigenvectors are evaluated by executing the eigenvalue decomposition on the correlation matrix. The eigenvectors are used as the basis vectors of class ω_i. The number of the basis vectors is the dimension of the subspace.

In the proposed method, the following simple similarity P_i is used:

$$P_i(\boldsymbol{x}) = \sum_{j=1}^{d_i} \left(\boldsymbol{x}^t \boldsymbol{u}_{ij}\right)^2, \tag{10}$$

where $\boldsymbol{x}$ is an unknown vector, $\boldsymbol{u}_{ij}$ is an eigenvector of each class, and d_i is the dimension to calculate the similarity, which is the number of significant basis vectors in subspace $\boldsymbol{Q}_i$.

4. Experiments

The tissues of coronary plaque are classified into the fibrous and lipid tissues. The classification performance of the proposed method by using the sparse coding is compared to that of the frequency analysis-based conventional method. In the proposed method and also the frequency analysis-based method, the window size of the local RF signal is 32

Table 1. Correct classification rates.

		Frequency analysis	Proposed method
Cross-sectional image 1	Fibrous tissue	0.98	0.92
	Lipid tissue	0.39	0.74
Cross-sectional image 2	Fibrous tissue	0.99	0.94
	Lipid tissue	0.49	0.77

points in depth and 4 lines in radial direction. The local RF signals are cut out from the learning signals only in the direction of depth however, we expand the window into two dimensions with both the depth and radial directions to take the neighboring information. In the sparse coding, the parameters β and M are set as 0.05 and 128, respectively. In the subspace method, the dimension d_i is all set as 20. In the the frequency analysis-based method, the KNN is used as the the classifier. The number of neighbors k is set as 9.

Table 1 shows the correct classification rates by each method. It is confirmed that the proposed method has good performance in both cases of the fibrous and lipid tissues. On the other hand, the frequency analysis-based method gives the low correct classification rates in the case of lipid tissue.

Figures 3 and 4 show the classification results for the fibrous and lipid tissues by each method. The yellow and green areas correspond to the fibrous and lipid tissues, respectively. The proposed method gives better results than the frequency analysis-based conventional method.

In the frequency analysis-based method, the combination of the power spectrum (as feature vectors) and the KNN (as a classifier) is used. Generally speaking, the KNN has higher classification ability than the subspace method. However, the classification results of the proposed method are better than the frequency analysis-based method. This seems to be a contradiction, but this is because the feature vectors obtained by the sparse coding are independent between each class, and those vectors have particular affinity to the subspace method. Further, the high speed tissue classification could be realized by the subspace method.

5. Conclusions

In this paper, we have proposed a novel method using sparse feature vectors obtained by applying sparse coding to the RF signal, for the tissue classification of plaque of the human coronary artery.

We realized, in our previous works, the accurate tissue characterization by using the feature vectors obtained by sparse coding with KNN. KNN however takes much time to calculate the distance between an unknown vector and the training vectors. In this paper, we focused on the independence of the feature vectors obtained by the sparse coding. Those feature vectors are considered to be independent between each class in the feature space. It was thus possible to perform the accurate tissue characterization in high-speed by using the subspace method with those feature vectors. The effectiveness of the proposed method was verified by comparing it with the conventional method.

Future work is to further improve the correct classification rate by introducing various pattern recognition methods.

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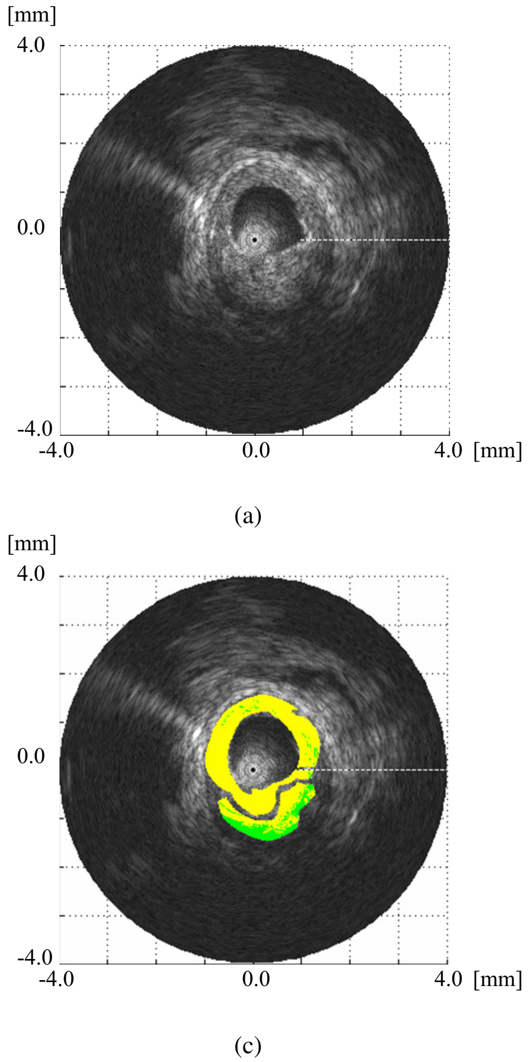

Fig. 3. Classification results for cross-sectional image 1. (a) B-mode image. (b) Medical doctor's findings. The yellow and green areas correspond to the fibrous and lipid tissues, respectively. (c) Results by the frequency analysis-based conventional method. (d) Results by the proposed method..

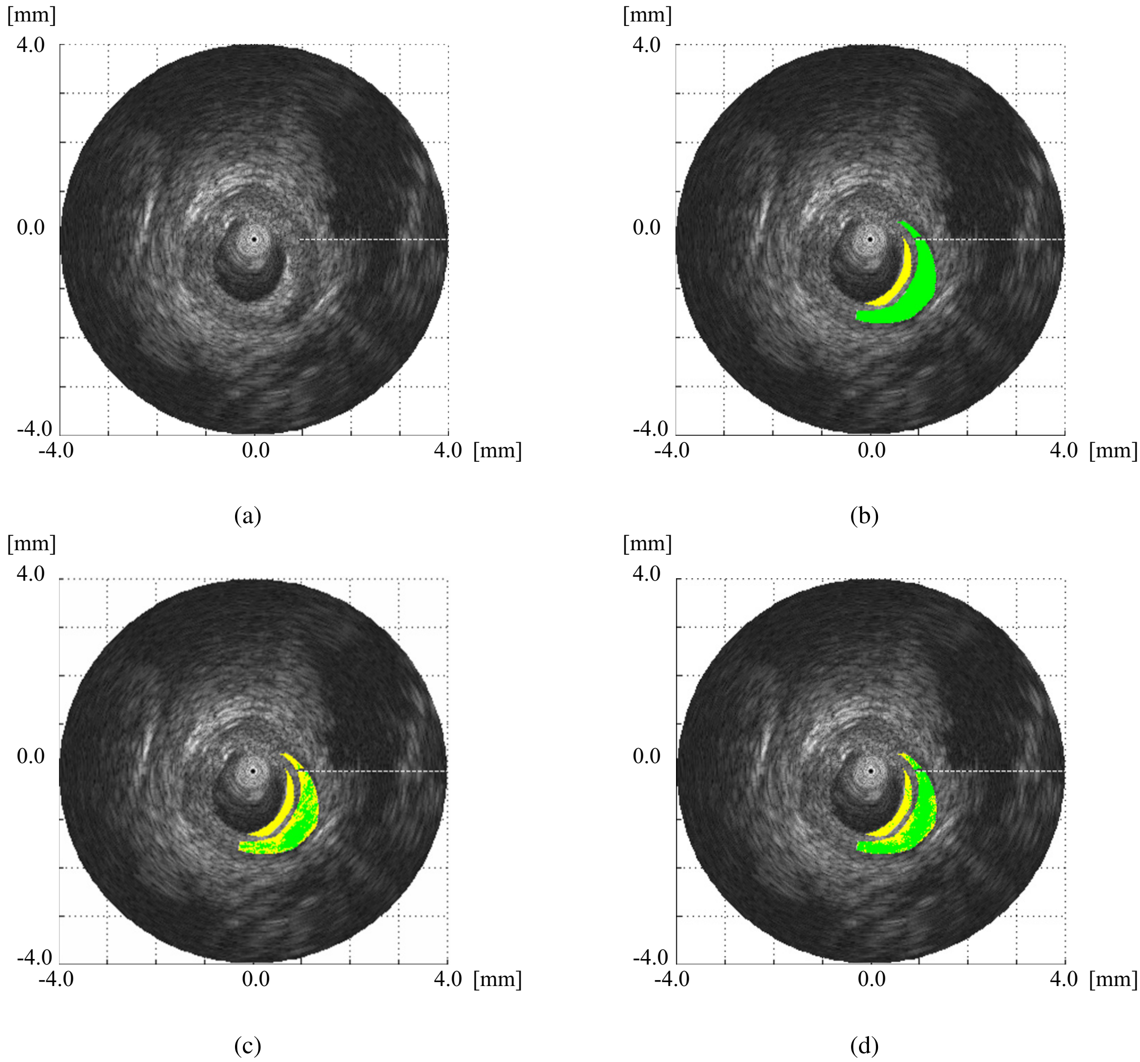

Fig. 4. Classification results for cross-sectional image 2. (a) B-mode image. (b) Medical doctor's findings. The yellow and green areas correspond to the fibrous and lipid tissues, respectively. (c) Results by the frequency analysis-based conventional method. (d) Results by the proposed method.

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